



## SEQUENCE LISTING

<1> RIEBEL, Bettina  
HUMMEL, Werner  
BOMMARIUS, Andreas

<120> RECOMBINANT ENZYMES HAVING IMPROVED NAD(H) ACCEPTANCE

<130> 210212US

<140> 09/910,033

<141> 2001-07-23

<150> DE 10037101.9

<151> 2000-07-27

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 759

<212> DNA

<213> Lactobacillus brevis

<220>

<221> CDS

<222> (1)..(759)

<223>

<400> 1

atg tct aac cgt ttg gat ggt aag gta gca atc att aca ggt ggt acg	48
Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Ile Thr Gly Gly Thr	
1 5 10 15	
ttg ggt atc ggt tta gct atc gcc acg aag ttc gtt gaa gaa ggg gct	96
Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala	
20 25 30	
aag gtc atg att acc gac cgg cac agc gat gtt ggt gaa aaa gca gct	144
Lys Val Met Ile Thr Asp Arg His Ser Asp Val Gly Glu Lys Ala Ala	
35 40 45	
aag agt gtc ggc act cct gat cag att caa ttt ttc caa cat gat tct	192
Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser	
50 55 60	
tcc gat gaa gac ggc tgg acg aaa tta ttc gat gca acg gaa aaa gcc	240
Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala	
65 70 75 80	
ttt ggc cca gtt tct aca tta gtt aat aac gct ggg atc gcg gtt aac	288
Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn	
85 90 95	
aag agt gtc gaa gaa acc acg act gct gaa tgg cgt aaa tta tta gcc	336

A1  
 Cont  
 Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala  
 100 105 110  
 gtc aac ctt gat ggt gtc ttc ttc ggt acc cga tta ggg att caa cgg 384  
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg  
 115 120 125  
 atg aag aac aaa ggc tta ggg gct tcc atc atc aac atg tct tcg atc 432  
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile  
 130 135 140  
 gaa ggc ttt gtg ggt gat cct agc tta ggg gct tac aac gca tct aaa 480  
 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys  
 145 150 155 160  
 ggg gcc gta cgg att atg tcc aag tca gct gcc tta gat tgt gcc cta 528  
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu  
 165 170 175  
 aag gac tac gat gtt cgg gta aac act gtt cac cct ggc tac atc aag 576  
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys  
 180 185 190  
 aca cca ttg gtt gat gac cta cca ggg gcc gaa gaa gcg atg tca caa 624  
 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln  
 195 200 205  
 cgg acc aag acg cca atg ggc cat atc ggt gaa cct aac gat att gcc 672  
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala  
 210 215 220  
 tac atc tgt gtt tac ttg gct tct aac gaa tct aaa ttt gca acg ggt 720  
 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly  
 225 230 235 240  
 tct gaa ttc gta gtt gac ggt ggc tac act gct caa tag 759  
 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln  
 245 250

<210> 2  
 <211> 252  
 <212> PRT  
 <213> Lactobacillus brevis

<400> 2

Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Ile Thr Gly Gly Thr  
 1 5 10 15

Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala  
 20 25 30

Lys Val Met Ile Thr Asp Arg His Ser Asp Val Gly Glu Lys Ala Ala  
 35 40 45

AI  
CONT

Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser  
50 55 60

Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala  
65 70 75 80

Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn  
85 90 95

Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala  
100 105 110

Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg  
115 120 125

Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile  
130 135 140

Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys  
145 150 155 160

Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu  
165 170 175

Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys  
180 185 190

Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln  
195 200 205

Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala  
210 215 220

Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly  
225 230 235 240

Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln  
245 250

<210> 3  
<211> 24  
<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA

<400> 3

accgaccggc acagcgatgt tggc

24

<210> 4

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 4

Thr Asp Arg His Ser Asp Val Gly

1

5

<210> 5

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA

<400> 5

accaacatcg ctgtgccggc cggt

24

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 6

Gly Val Asp Ser His Arg Asp Thr

1

5

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

AI  
cont

<400> 7

Thr Asp Arg His Ser Asp Val Gly  
1 5